

Lee, Li

1645

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/305,984B

DATE: 03/03/2000
TIME: 12:53:52

Input Set: I305984B.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

PS

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1 <110> APPLICANT: Novak, Rodger
2 Toumanen, Elaine
3 <120> TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
4 <130> FILE REFERENCE: 1340-1-016N1
5 <140> CURRENT APPLICATION NUMBER: US/09/305,984B
6 <141> CURRENT FILING DATE: 1999-05-05
7 <150> EARLIER APPLICATION NUMBER: 60/084,399
8 <151> EARLIER FILING DATE: 1998-05-06
9 <150> EARLIER APPLICATION NUMBER: 09/305,984
10 <151> EARLIER FILING DATE: 1999-05-05
11 <160> NUMBER OF SEQ ID NOS: 76
12 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 75
15 <212> TYPE: DNA
16 <213> ORGANISM: Streptococcus pneumoniae
17 <400> SEQUENCE: 1
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19 gcaagagact ataat 75
20 <210> SEQ ID NO 2
21 <211> LENGTH: 25
22 <212> TYPE: PRT
23 <213> ORGANISM: Streptococcus pneumoniae
24 <400> SEQUENCE: 2
25 Met Arg Lys Glu Phe His Asn Val Leu Ser Ser Gly Gln Leu Leu Ala
26 1 5 10 15
27 Asp Lys Arg Pro Ala Arg Asp Tyr Asn
28 20 25
29 <210> SEQ ID NO 3
30 <211> LENGTH: 75
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Description of Artificial Sequence: Encodes
35 modified Streptococcus Pneumonia peptide
36 <400> SEQUENCE: 3
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38 gcaagagact ataat 75
39 <210> SEQ ID NO 4
40 <211> LENGTH: 25
41 <212> TYPE: PRT
42 <213> ORGANISM: Artificial Sequence
43 <220> FEATURE:
44 <223> OTHER INFORMATION: Description of Artificial Sequence: Modified

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45      Streptococcus Pneumonia peptide
46  <400> SEQUENCE: 4
47      Met Arg Lys Glu Phe His Asn Val Leu Ser Ala Gly Gln Leu Leu Ala
48          1              5              10              15
49      Asp Lys Arg Pro Ala Arg Asp Tyr Asn
50          20              25
51  <210> SEQ ID NO 5
52  <211> LENGTH: 75
53  <212> TYPE: DNA
54  <213> ORGANISM: Artificial Sequence
55  <220> FEATURE:
56  <223> OTHER INFORMATION: Description of Artificial Sequence: Encodes
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58  <400> SEQUENCE: 5
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60      gcaagagacg ctaat                                     75
61  <210> SEQ ID NO 6
62  <211> LENGTH: 25
63  <212> TYPE: PRT
64  <213> ORGANISM: Artificial Sequence
65  <220> FEATURE:
66  <223> OTHER INFORMATION: Description of Artificial Sequence: Modified
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68  <400> SEQUENCE: 6
69      Met Arg Lys Glu Phe His Asn Val Leu Ser Ser Gly Gln Leu Leu Ala
70          1              5              10              15
71      Asp Lys Arg Pro Ala Arg Asp Ala Asn
72          20              25
73  <210> SEQ ID NO 7
74  <211> LENGTH: 42
75  <212> TYPE: DNA
76  <213> ORGANISM: Streptococcus pneumoniae
77  <400> SEQUENCE: 7
78      atgagaaagg aatttcacaa cgttttatct agtgggtcagt tg                                     42
79  <210> SEQ ID NO 8
80  <211> LENGTH: 14
81  <212> TYPE: PRT
82  <213> ORGANISM: Streptococcus pneumoniae
83  <400> SEQUENCE: 8
84      Met Arg Lys Glu Phe His Asn Val Leu Ser Ser Gly Gln Leu
85          1              5              10
86  <210> SEQ ID NO 9
87  <211> LENGTH: 33
88  <212> TYPE: DNA
89  <213> ORGANISM: Streptococcus pneumoniae
90  <400> SEQUENCE: 9
91      cttgcagaca aaaggccagc aagagactat aat                                     33
92  <210> SEQ ID NO 10
93  <211> LENGTH: 11
94  <212> TYPE: PRT

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95 <213> ORGANISM: Streptococcus pneumoniae
96 <400> SEQUENCE: 10
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98       1             5             10
99 <210> SEQ ID NO 11
100 <211> LENGTH: 84
101 <212> TYPE: DNA
102 <213> ORGANISM: Streptococcus pneumoniae
103 <400> SEQUENCE: 11
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105   aaaaggccag caagagacta taat                                     84
106 <210> SEQ ID NO 12
107 <211> LENGTH: 28
108 <212> TYPE: PRT
109 <213> ORGANISM: Streptococcus pneumoniae
110 <400> SEQUENCE: 12
111   Met Glu Phe Met Arg Lys Glu Phe His Asn Val Leu Ser Ser Gly Gln
112       1             5             10             15
113   Leu Leu Ala Asp Lys Arg Pro Ala Arg Asp Tyr Asn
114       20             25
115 <210> SEQ ID NO 13
116 <211> LENGTH: 1329
117 <212> TYPE: DNA
118 <213> ORGANISM: Streptococcus pneumoniae
119 <400> SEQUENCE: 13
120   atgaaacgaa caggtttatt tgcaaagata tttatctata ccttctcgat atttagtctt 60
121   ctgggttatct gccttcattt agctatttat tttctttttc cttcgactta tctgagtcac 120
122   cgtcaggaaa ccattgggtca aaaggcaaca gccattgccc agtccctaga agggaaagat 180
123   aggagagta tctagcaagt gtttagacttg tattcccaga ctagtgatat caaggggacc 240
124   gtcaaagggtg agatgaccga ggacaagtta gaagtcaagg acagtcttcc tctggacaca 300
125   gaccgccaga caacctctct ctttattgag gagcgcgagg tgaaaacgca agacggtggt 360
126   actatgattc tccagtttct agcttccatg gatttacaaa aggaagcgga gcaaatcagt 420
127   ctccagtttc ttcctatac cttgctggcc tcttttctga tttccctttt ggtggcctac 480
128   atctacgtc ggactattgt tgcaccgatt ttggaaatca agcgggtgac ccgtcggatg 540
129   atggacctgg attcccaagt gcgattgcgc gtggattcta aggatgagat aggtaatctc 600
130   aaggaacaaa tcaatagcct ctaccagcat ctcttgactg ttattgcgga cttgcatgaa 660
131   aagaatgaag ccattctcca gctggagaag atgaaggtcg aattcctacg aggagcttct 720
132   catgaattga aaacaccgct ggctagtttg aaaatcctaa tcgaaaatat gagagagaat 780
133   atcggtcggt ataaggatag agaccagtat ctgggagttg ccttggggat tgtggatgaa 840
134   ctcaatcacc atgttctgca gatactttcc ctctcttctg tgcaggaatt gcgagatgat 900
135   agggaaacaa ttgacctcct ccagatgacg caaaatctgg tcaaagatta tgccttgcta 960
136   gccaaaggaaa gagagctcca gatagacaat agtttgaccc atcagcaggc ttatctaaac 1020
137   ccatcagtta tgaagttgat tctttctaata ctcatcagca atgccattaa gcactctgtt 1080
138   ccaggtggct tagttcgaat tggagaaaga gaaggagaac tttttatcga aaatagctgt 1140
139   agctcagagg aacaagaaaa actagcccag tctttttctg acaatgccag tcgcaagggtc 1200
140   aaggggtctg gtatggggct ctttgtgggt aagagtctat tagaacatga aaaattagct 1260
141   tatcgtttcg agatggagga gaatagttta accttcttta tagattttcc aaaagtcgtc 1320
142   caagactag                                     1329
143 <210> SEQ ID NO 14
144 <211> LENGTH: 442

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145 <212> TYPE: PRT
146 <213> ORGANISM: Streptococcus pneumoniae
147 <400> SEQUENCE: 14
148 Met Lys Arg Thr Gly Leu Phe Ala Lys Ile Phe Ile Tyr Thr Phe Ser
149 1 5 10 15
150 Ile Phe Ser Val Leu Val Ile Cys Leu His Leu Ala Ile Tyr Phe Leu
151 20 25 30
152 Phe Pro Ser Thr Tyr Leu Ser His Arg Gln Glu Thr Ile Gly Gln Lys
153 35 40 45
154 Ala Thr Ala Ile Ala Gln Ser Leu Glu Gly Lys Asp Arg Gln Ser Ile
155 50 55 60
156 Glu Gln Val Leu Asp Leu Tyr Ser Gln Thr Ser Asp Ile Lys Gly Thr
157 65 70 75 80
158 Val Lys Gly Glu Met Thr Glu Asp Lys Leu Glu Val Lys Asp Ser Leu
159 85 90 95
160 Pro Leu Asp Thr Asp Arg Gln Thr Thr Ser Leu Phe Ile Glu Glu Arg
161 100 105 110
162 Glu Val Lys Thr Gln Asp Gly Gly Thr Met Ile Leu Gln Phe Leu Ala
163 115 120 125
164 Ser Met Asp Leu Gln Lys Glu Ala Glu Gln Ile Ser Leu Gln Phe Leu
165 130 135 140
166 Pro Tyr Thr Leu Leu Ala Ser Phe Leu Ile Ser Leu Leu Val Ala Tyr
167 145 150 155 160
168 Ile Tyr Ala Arg Thr Ile Val Ala Pro Ile Leu Glu Ile Lys Arg Val
169 165 170 175
170 Thr Arg Arg Met Met Asp Leu Asp Ser Gln Val Arg Leu Arg Val Asp
171 180 185 190
172 Ser Lys Asp Glu Ile Gly Asn Leu Lys Glu Gln Ile Asn Ser Leu Tyr
173 195 200 205
174 Gln His Leu Leu Thr Val Ile Ala Asp Leu His Glu Lys Asn Glu Ala
175 210 215 220
176 Ile Leu Gln Leu Glu Lys Met Lys Val Glu Phe Leu Arg Gly Ala Ser
177 225 230 235 240
178 His Glu Leu Lys Thr Pro Leu Ala Ser Leu Lys Ile Leu Ile Glu Asn
179 245 250 255
180 Met Arg Glu Asn Ile Gly Arg Tyr Lys Asp Arg Asp Gln Tyr Leu Gly
181 260 265 270
182 Val Ala Leu Gly Ile Val Asp Glu Leu Asn His His Val Leu Gln Ile
183 275 280 285
184 Leu Ser Leu Ser Ser Val Gln Glu Leu Arg Asp Asp Arg Glu Thr Ile
185 290 295 300
186 Asp Leu Leu Gln Met Thr Gln Asn Leu Val Lys Asp Tyr Ala Leu Leu
187 305 310 315 320
188 Ala Lys Glu Arg Glu Leu Gln Ile Asp Asn Ser Leu Thr His Gln Gln
189 325 330 335
190 Ala Tyr Leu Asn Pro Ser Val Met Lys Leu Ile Leu Ser Asn Leu Ile
191 340 345 350
192 Ser Asn Ala Ile Lys His Ser Val Pro Gly Gly Leu Val Arg Ile Gly
193 355 360 365
194 Glu Arg Glu Gly Glu Leu Phe Ile Glu Asn Ser Cys Ser Ser Glu Glu

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195          370          375          380
196      Gln Glu Lys Leu Ala Gln Ser Phe Ser Asp Asn Ala Ser Arg Lys Val
197          385          390          395          400
198      Lys Gly Ser Gly Met Gly Leu Phe Val Val Lys Ser Leu Leu Glu His
199          405          410          415
200      Glu Lys Leu Ala Tyr Arg Phe Glu Met Glu Glu Asn Ser Leu Thr Phe
201          420          425          430
202      Phe Ile Asp Phe Pro Lys Val Val Gln Asp
203          435          440
204 <210> SEQ ID NO 15
205 <211> LENGTH: 657
206 <212> TYPE: DNA
207 <213> ORGANISM: Streptococcus pneumoniae
208 <400> SEQUENCE: 15
209      atgaaaattt taattgtaga agatgaagag atgatccgtg aggggggtcag tgattatttg 60
210      acggattgtg gctatgaaac tattgaggca gcggacggtc aggaagctct ggagcaattt 120
211      tctagctatg aggtggccct ggttttactg gatatccaga tgcccaagct caacggctta 180
212      gaagtccctag ctgagattcg taaaaccagt caggttcctg tcttgatgtt gacagctttt 240
213      caagatgagg aatacaagat gaggtccttt gcctcttttg cagatggcta tctggaaaaa 300
214      cctttctccc tctccctttt aaaagtgagg gtggacgcga ttttcaagcg ctactacgat 360
215      acaggacgaa tcttttctta caaggatacc aagggtggact ttgaaagcta cagtgcagc 420
216      ctgcaggtc aagaagtgcc tatcaatgcc aaagagttgg aaattctgga ctatctagt 480
217      aaaaatgaag gccgggcctt gactcgatct cagattatcg atgccgtctg gaaagcgaca 540
218      gatgaggttc cctttgaccg tgttattgat gtttatatca aggaattgcg gaaaaagcta 600
219      gacttggtt gtatcctcac tgtgcgcaat gttggttata aattggagcg aaaatga 657
220 <210> SEQ ID NO 16
221 <211> LENGTH: 218
222 <212> TYPE: PRT
223 <213> ORGANISM: Streptococcus pneumoniae
224 <400> SEQUENCE: 16
225      Met Lys Ile Leu Ile Val Glu Asp Glu Glu Met Ile Arg Glu Gly Val
226          1          5          10          15
227      Ser Asp Tyr Leu Thr Asp Cys Gly Tyr Glu Thr Ile Glu Ala Ala Asp
228          20          25          30
229      Gly Gln Glu Ala Leu Glu Gln Phe Ser Ser Tyr Glu Val Ala Leu Val
230          35          40          45
231      Leu Leu Asp Ile Gln Met Pro Lys Leu Asn Gly Leu Glu Val Leu Ala
232          50          55          60
233      Glu Ile Arg Lys Thr Ser Gln Val Pro Val Leu Met Leu Thr Ala Phe
234          65          70          75          80
235      Gln Asp Glu Glu Tyr Lys Met Ser Ala Phe Ala Ser Leu Ala Asp Gly
236          85          90          95
237      Tyr Leu Glu Lys Pro Phe Ser Leu Ser Leu Leu Lys Val Arg Val Asp
238          100          105          110
239      Ala Ile Phe Lys Arg Tyr Tyr Asp Thr Gly Arg Ile Phe Ser Tyr Lys
240          115          120          125
241      Asp Thr Lys Val Asp Phe Glu Ser Tyr Ser Ala Ser Leu Ala Gly Gln
242          130          135          140
243      Glu Val Pro Ile Asn Ala Lys Glu Leu Glu Ile Leu Asp Tyr Leu Val
244          145          150          155          160

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION US/09/305,984BDATE: 03/03/2000
TIME: 12:53:52

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| 823 | W "N" or "Xaa" used: Feature required | Asp Lys Arg Pro Ala Arg Asp Xaa Asn |
| 861 | W "N" or "Xaa" used: Feature required | Arg Lys Glu Phe His Xaa Xaa Xaa Xaa Xaa X |
| 863 | W "N" or "Xaa" used: Feature required | Lys Arg Pro Xaa Arg Asp Tyr |
| 914 | W "N" or "Xaa" used: Feature required | Met Xaa Xaa Xaa Xaa Xaa Asn Val Leu Ser X |
| 916 | W "N" or "Xaa" used: Feature required | Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Asn |
| 1028 | W "N" or "Xaa" used: Feature required | Xaa Ser Gly Gly Xaa |